



```

Db 61 FFKGTATLPIIFHQQVSPILFGLLAVIGHTFFIFAGFKGKAVATSGVIFGAPIF 120
QY 61 FFKGTATLPIIFHQQVSPILFGLLAVIGHTFFIFAGFKGKAVATSGVIFGAPIF 120
Db 121 CLYLAIFFGALYLGSMISLSSVTASIAAVIGVLLPFLFGFILTSLNYDSELFATIALASL 180
QY 121 CLYLAIFFGALYLGSMISLSSVTASIAAVIGVLLPFLFGFILTSLNYDSELFATIALASL 180
Db 181 IIRHKDNIARIKNTENLPVGNLTHODPKK 213
QY 181 IIRHKDNIARIKNTENLPVGNLTHODPKK 213

RESULT 2
ID YNES_BACSU STANDARD; PRT: 193 AA.
AC Q45064:
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE HYPOTHETICAL 21.0 KD PROTEIN IN TLP-GRLB INTERGENIC REGION.
GN YNES.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168:
RA ROSE M., ENTIAN K.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE UPF0078 FAMILY.
CC
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CC
CC EMBL: Z73234; CAA97604.1;
CC EMBL: Z99113; CABI3690.1;
CC DR SUBLIST: BG11826; YNES.
CC KW Hypothetical protein; Transmembrane.
FT TRANSMEM 2 22 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 111 131 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
SQ SEQUENCE 193 AA; 20966 MW; BC042392 CRC32;

Query Match 39.9%; Score 616; DB 1; Length 193;
Best Local Similarity 50.0%; Pred. No. 4.10e-65;
Matches 101; Conservative 45; Mismatches 46; Indels 10; Gaps 6;

Db 1 MLTALIIILAYLGSTPSGLVCKLAGIDIREHSGNIGATNAFTLGKAGSVVIAGD 60
QY 1 MITIVLLIILAYLGSTPSGLVCKLAGIDIREHSGNIGATNAFTLGKAGSVVIAGD 60
Db 61 ILKGTATLPIIFHQQVSPILFGLLAVIGHTFFIFAGFKGKAVATSGVLLFPAPLL 119
QY 61 FFKGTATLPIIFHQQVSPILFGLLAVIGHTFFIFAGFKGKAVATSGVIFGAPIF 120
Db 120 FIFMAVFIFLTKFVSLSSMLTGIVTIV---YS-F-FVHDTY--LLIVTL-LTIF 170
QY 121 CLYLAIFFGALYLGSMISLSSVTASIAAVIGVLLPFLFGFILTSLNYDSELFATIALASL 180
Db 171 VIYHRANIKRIINKTEPKVK 192
QY 181 IIRHKDNIARIKNTENLPV 202

RESULT 3

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ID Y676_AQUAE STANDARD; PRT: 192 AA.
AC O66905;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE HYPOTHETICAL PROTEIN AQ_676.
GN AQ_676.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RC MEDLINE: 98196666.
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE UPF0078 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: A800701; AAC06869.1;
CC KW Hypothetical protein; Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 51 71 POTENTIAL.
FT TRANSMEM 80 100 POTENTIAL.
FT TRANSMEM 112 132 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
SQ SEQUENCE 192 AA; 20940 MW; CB7A57E2 CRC32;

Query Match 29.8%; Score 460; DB 1; Length 192;
Best Local Similarity 42.6%; Pred. No. 1.59e-43;
Matches 83; Conservative 55; Mismatches 43; Indels 14; Gaps 13;

Db 1 MKALFLVIFAYLGLSITFGEVIAKLGVDLRNVGSGNVGATNTRALGRKRYGLVFLFD 59
QY 1 MITIVLLIILAYLGSTPSGLVCKLAGIDIREHSGNIGATNAFTLGKAGSVVIAGD 60
Db 60 FLKGFIPALIAVKSGIDS-WLFTGLASVLGHMYPVFFGFKGKGVATAGLVFAVSP 118
QY 61 FFKGTATLPIIFHQQVSPILFGLLAVIGHTFFIFAGFKGKAVATSGVIFGAP 118
Db 119 SVAFSLFVLWLG-IPLMKRYVSLASITATISA-F-LFLF-VAGYPV-N--VLFNAIVIG- 170
QY 119 IFCLYLAIFFGALYLGSMISLSSVTASIAAVIGVLLPFLFGFILTSLNYDSELFATIAL 177
Db 171 A-LIYHRENINRL 184
QY 178 ASLIIIRHKDNIARI 192

RESULT 4
ID YJ73_SYNY3 STANDARD; PRT: 222 AA.
AC Y73933;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE HYPOTHETICAL 23.5 KD PROTEIN SLL1973.
GN SLL1973.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 97061201.

```

RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,  
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,  
RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,  
RA TABATA S.,  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT *Synechocystis* sp. strain PC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO THE UPF0078 FAMILY.  
CC -----  
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CC -----  
DR EMBL: D90910; BAAL7999.1;  
FT TRANSMEM 4 24 POTENTIAL.  
FT TRANSMEM 56 76 POTENTIAL.  
FT TRANSMEM 87 107 POTENTIAL.  
FT TRANSMEM 130 150 POTENTIAL.  
FT TRANSMEM 153 173 POTENTIAL.  
SQ SEQUENCE 222 AA; 23534 MW; D5B6F852 CRC32;  
  
Query Match 22.9%; Score 354; DB 1; Length 222;  
Best Local Similarity 39.2%; Pred. No. 2.75e-29;  
Matches 82; Conservative 56; Mismatches 50; Indels 21; Gaps 17;  
  
Db 6 LKCLLLIYLGMSIPTGYLAGLLGIDIREHSGSKGTATNVFRTLGKPAALAVLAD 65  
QY 1 MITIVLLIAYLGSGISGLWIGOVFFQINLREHSGSGTGTNTFRILGKAGKAGATEVID 60  
  
Db 66 ISKGVAVAVLRAIYSGDMDPALPAQWNLTLGVAIVLGHSGSKSIFLFGSKSVATS 125  
QY 61 FFKGTLA-TLLPIF--H-LOGV-SP---LIFGL-LAVI-GHTFPFAGFGKGVATS 109  
  
Db 126 LGVLFMNIWALGTLAT-FLTVIFFTRIVSLSSIVAIA-VNGIAL-AL-Q-LPPPYLA 180  
QY 110 AGVIFGAPIFCL-YLAIFFGALYLGSMISLSSVTASIAVIGLVLLFPLFGFSLNSYS 168  
  
Db 181 -F-TF-LA-GMYIVVRHTNIERTLOCTE 205  
QY 169 LFIAIILASLIIIRHKDNIARKNKTE 197  
  
RESULT 5  
ID YGIH\_ECOLI STANDARD; PRT; 205 AA.  
AC P31056;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE HYPOTHETICAL 22.2 KD PROTEIN IN BACA-TTDA INTERGENIC REGION (0205).  
GN YGIH.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE; 97426617.  
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,  
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,  
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,  
RA MAU B., SHAO Y.;  
RT "The complete genome sequence of *Escherichia coli* K-12.";  
RT Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE OF 1-204 FROM N.A.

RC STRAIN-JM83;  
RX MEDLINE; 93285992.  
RA CAIN B.D., NORTON P.J., EUBANKS W., NICK H.S., ALLEN C.M.;  
RT "Amplification of the *bacA* gene confers bacitracin resistance to  
RT *Escherichia coli*.";  
RL J. Bacteriol. 175:3784-3789(1993).  
RN [3]  
RP IDENTIFICATION.  
RX MEDLINE; 95075659.  
RA BORODOVSKY M., RUDD K.E., KOONIN E.V.;  
RT "Intrinsic and extrinsic approaches for detecting genes in a  
RT bacterial genome.";  
RL Nucleic Acids Res. 22:4756-4767(1994).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO THE UPF0078 FAMILY. STRONG, TO H.INFLUENZAE  
CC HI0266.  
CC -----  
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CC -----  
DR EMBL: U28379; AAA89139.1;  
DR EMBL: AE000387; AAC76095.1;  
DR EMBL: L12966; NOT\_ANNOTATED\_CDS.  
DR ECOGENE; EGI1674; YGIH.  
KW Hypothetical protein; Transmembrane.  
FT TRANSMEM 4 24 POTENTIAL.  
FT TRANSMEM 53 73 POTENTIAL.  
FT TRANSMEM 82 102 POTENTIAL.  
FT TRANSMEM 112 132 POTENTIAL.  
FT TRANSMEM 138 158 POTENTIAL.  
SQ SEQUENCE 205 AA; 22193 MW; FE3A2166 CRC32;  
  
Query Match 19.2%; Score 297; DB 1; Length 205;  
Best Local Similarity 36.3%; Pred. No. 7.28e-22;  
Matches 74; Conservative 56; Mismatches 57; Indels 17; Gaps 13;  
  
Db 4 IAPGMILAIYCGSISAILVCRICGLDPDRTSGSNPGATNVLRIKGGKAAVAVLFDV 63  
QY 2 ITIVLLIAYLGSGISGLWIGOVFFQINLREHSGSGTGTNTFRILGKAGKAGATEVID 61  
  
Db 64 LKGMPL-VWCA-YEL-GVSPFWLGLIAACLGHIWPFVFGKGVATFAGAI---AP 117  
QY 62 FKGTLATLPIIFHLOGVSLIFGLAV---IGHTFPIFAGFGKGVATFAGVIFGFAP 118  
  
Db 118 IG-WDLTGVNAGT-WLLTVL-LSGYS-SLGAIVSALIAP-F-YVWV-FKQFTFPVSMLS 170  
QY 119 IFCLYLAIFFGALYLGSMISLSSVTASIAVIGLVLLFPLFGFSLNSYDSLFAIILALA 178  
  
Db 171 CLILLRHNDNIQRLWRQETKI-W 193  
QY 179 SLIIIRHKDNIARKNKTNLVPW 202  
  
RESULT 6  
ID YGIH\_HAEM STANDARD; PRT; 199 AA.  
AC P44603;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE HYPOTHETICAL PROTEIN HI0266.  
GN HI0266.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-RD / KW20;  
RX MEDLINE; 95350630.



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DR EMBL: U39703; AAC71467.1; -  
 DR TIGR: MG247; -  
 KW Hypothetical protein: Transmembrane.  
 FT TRANSMEM 7 27 POTENTIAL.  
 FT TRANSMEM 61 81 POTENTIAL.  
 FT TRANSMEM 99 119 POTENTIAL.  
 FT TRANSMEM 135 155 POTENTIAL.  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT TRANSMEM 199 219 POTENTIAL.  
 SQ SEQUENCE 239 AA; 27489 MW; 2CBEFCEFCRC32;

Query Match 12.2%; Score 188; DB 1; Length 239;  
 Best Local Similarity 31.3%; Pred. No. 1.75e-08;  
 Matches 62; Conservative 53; Mismatches 49; Indels 22; Gaps 15;

Db 9 ILVIFSLAGYLGSIIADI-FSKIL-KKVRFGSKNPGATNSMRVFGKIGFLVAIP 66  
 QY 2 ITIVL-LILAYLGSIP-SGLWIGQVFFQINLREHSGNTGTTNTRILCKKAGMATFVI 59  
 Db 67 DAFKGFAPLTLWILRFGLGVLTEKVVOSTYFLVLSCFRATIGHIPLFKFKGKA 126  
 QY -60 DFKGTLATLP-IIFH-LQG-VSLPIF-G---L-L---AVIGHTPFIAGFKGKA 105  
 Db 127 IATGGSLLAISLWMLICLLIMITL-ITKYVSLASLVTFFVLAV-IILVPLWLDYLF 184  
 QY 106 VATSAGVIFGFAPF-FCLYLAIFFGALYGLSMISLSSVTASIAAIGVLLPLFGFI-L 163  
 Db 185 FNSDPL 190  
 QY 164 SNYDSL 169

RESULT 9  
 ID Y247\_MYCPN STANDARD; PRT; 239 AA.  
 AC P75428;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE HYPOTHETICAL PROTEIN MG247 HOMOLOG.  
 OS Mycoplasma pneumoniae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Mycoplasmataceae; Mycoplasma.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 29342 / M129;  
 RX MEDLINE; 97105885.  
 RA HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,  
 RA HERRMANN R.;  
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
 RT pneumoniae";  
 RL Nucleic Acids Res. 24:4420-4449(1996).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0078 FAMILY.

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DR EMBL: AE000047; AB96134.1; -  
 KW Hypothetical protein; Transmembrane.  
 FT TRANSMEM 6 26 POTENTIAL.  
 FT TRANSMEM 62 82 POTENTIAL.

FT TRANSMEM 99 119 POTENTIAL.  
 FT TRANSMEM 135 155 POTENTIAL.  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT TRANSMEM 199 219 POTENTIAL.  
 SQ SEQUENCE 239 AA; 27439 MW; 58287C2D CRC32;

Query Match 10.2%; Score 158; DB 1; Length 239;  
 Best Local Similarity 31.3%; Pred. No. 4.06e-05;  
 Matches 55; Conservative 53; Mismatches 47; Indels 21; Gaps 13;

Db 11 IVFSLVIGYMGVMFADY-FOKIL-NKDVRKLGSKNPGATNSIRVFGKIGFLVGLCDA 68  
 QY 4 IIVL-LILAYLGSIP-SGLWIGQVFFQINLREHSGNTGTTNTRILCKKAGMATFVIDF 61  
 Db 69 LAGFLAFVFSFLIFSWLQOYLNVNQYKVVYLTLSLSCFAATIGHIPLFKFKGKA 128  
 QY 62 FKGTATLTP-IIFH-LQ---GVSP-L---L---AVIGHTPFIAGFKGKA 107  
 Db 129 TFGGSLAISLWMLICLLIMITL-ITKYVSLASLVTFFVLAV-IILVPLWLDYLF 182  
 QY 108 TSGVIFGFAPF-FCLYLAIFFGALYGLSMISLSSVTASIAAIGVLLPLFGFI 162

RESULT 10  
 ID NAHI\_MOUSE STANDARD; PRT; 820 AA.

AC Q61165;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE SODIUM/HYDROGEN EXCHANGER 1 (NA(+)/H(+)) EXCHANGER 1) (NHE-1).  
 GN SLC9A1 OR NHE1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RA DEWEY M.J., BOWMAN L.H.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED  
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL  
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD  
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL  
 CC TRANSDUCTION.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED (POSSIBLE).  
 CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+)) EXCHANGER FAMILY.  
 CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC  
 CC DOMAINS IN THE NA(+)/H(+)) EXCHANGERS VARY AMONG AUTHORS.  
 CC -1- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE  
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DR EMBL: U51112; AAA92976.1;  
 DR MGD; MGI:102462; SLC9A1.  
 DR PFAM: PF00959; Na.H.Exchanger; 1.  
 KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;  
 KW Multigene family; Phosphorylation.  
 FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 13 32 A (M1) HYDROPHOBIC.  
 FT DOMAIN 33 105 CVTOLPLASMIC (POTENTIAL).  
 FT DOMAIN 106 127 B (M2) HYDROPHOBIC.  
 FT DOMAIN 128 130 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 131 150 C (M3) (POTENTIAL).  
 FT DOMAIN 151 162 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 163 183 D (M4) (POTENTIAL).

```

FT DOMAIN 184 188 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 189 210 E (M5) (POTENTIAL).
FT DOMAIN 211 230 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 231 251 F (M5A) (POTENTIAL).
FT DOMAIN 252 260 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 261 282 G (M5B) (POTENTIAL).
FT DOMAIN 283 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 322 H (M6) (POTENTIAL).
FT DOMAIN 323 337 I (M7) (POTENTIAL).
FT TRANSMEM 338 357 J (M8) (POTENTIAL).
FT DOMAIN 358 388 K (M9) (POTENTIAL).
FT TRANSMEM 389 410 L (M10) (POTENTIAL).
FT DOMAIN 411 416 L, HYDROPHOBIC.
FT TRANSMEM 417 438 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 439 452 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 453 473 M (M10) (POTENTIAL).
FT DOMAIN 474 482 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 483 503 M (M10) (POTENTIAL).
FT DOMAIN 504 820 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 374 374 POTENTIAL.
SQ SEQUENCE 820 AA; 91467 MW; CB3788F4 CRC32;

Query Match 9.4%; Score 145; DB 1; Length 820;
Best Local Similarity 27.3%; Pred. No. 9.97e-04;
Matches 36; Conservative 40; Mismatches 45; Indels 11; Gaps 9;

Db 262 LVFGESLLNDATVVLVHLFEFASVDSVGSID-IFLGFLSFFVVALGGVGVVY-GVI 319
QY 82 LIFG--LL--AVIGHTFPFAGKGVAVTSAGVIFGAPICFLYLAIFFGALYLSM 137
Db 320 AARTSRTSHIRVIEPLVF-LVSYMAYLSAEFLHSGIMALIASGVVMPYVE-ANISH 377
QY 138 ISLSS-VTASIAAVIGVLLPFLGFLSNDLSL-IAIILAL-ASLIIRHKDNIARIKN 194
Db 378 KSHTTIKYELKM 389
QY 195 KTENLVPWGLNL 206

RESULT - 11
ID NAHL_BOVIN STANDARD; PRT; 817 AA.
AC 028036;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE SODIUM/HYDROGEN EXCHANGER 1 (NA(+)/H(+)) EXCHANGER 1 (NHE-1).
GN SLC9A1 OR NHE1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA ZHU H., ZHANG Q., ZHANG X., LIU W., TRUMBLY R.J., GARLID K.D.,
RA SUN X.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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CC -----
CC EMBL: U49432; AAA91483.1;
CC PFAM: PF00999; Na_H_Exchange; 1.
CC Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
CC Multigene family; Phosphorylation.
CC DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 16 35 M1 (POTENTIAL).
CC DOMAIN 36 107 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 108 127 M2 (POTENTIAL).
CC DOMAIN 128 129 M3 (POTENTIAL).
CC TRANSMEM 130 149 M4 (POTENTIAL).
CC DOMAIN 150 154 M5 (POTENTIAL).
CC TRANSMEM 155 174 M6 (POTENTIAL).
CC DOMAIN 175 191 M7 (POTENTIAL).
CC TRANSMEM 192 211 M8 (POTENTIAL).
CC DOMAIN 212 227 M9 (POTENTIAL).
CC TRANSMEM 228 247 M10 (POTENTIAL).
CC DOMAIN 248 256 M11 (POTENTIAL).
CC TRANSMEM 257 276 M12 (POTENTIAL).
CC DOMAIN 277 294 M13 (POTENTIAL).
CC TRANSMEM 295 315 M14 (POTENTIAL).
CC DOMAIN 316 338 M15 (POTENTIAL).
CC TRANSMEM 339 358 M16 (POTENTIAL).
CC DOMAIN 359 386 M17 (POTENTIAL).
CC TRANSMEM 387 406 M18 (POTENTIAL).
CC DOMAIN 407 410 M19 (POTENTIAL).
CC TRANSMEM 411 430 M20 (POTENTIAL).
CC DOMAIN 431 480 M21 (POTENTIAL).
CC TRANSMEM 481 500 M22 (POTENTIAL).
CC DOMAIN 501 817 M23 (POTENTIAL).
CC CARBOHYD 75 75 POTENTIAL.
CC CARBOHYD 370 370 POTENTIAL.
SQ SEQUENCE 817 AA; 91017 MW; 42535859 CRC32;

Query Match 9.2%; Score 142; DB 1; Length 817;
Best Local Similarity 27.3%; Pred. No. 2.05e-03;
Matches 36; Conservative 37; Mismatches 48; Indels 11; Gaps 9;

Db 258 LVFGESLLNDATVVLVHLFEFASVDSVGSID-IFLGFLSFFVVALGGVGVVY-GVI 315
QY 82 LIFG--LL--AVIGHTFPFAGKGVAVTSAGVIFGAPICFLYLAIFFGALYLSM 137
Db 316 AARTSRTSHIRVIEPLVF-LVSYMAYLSAEFLHSGIMALIASGVVMPYVE-ANISH 373
QY 138 ISLSS-VTASIAAVIGVLLPFLGFLSNDLSL-IAIILAL-ASLIIRHKDNIARIKN 194
Db 374 KSHTTIKYELKM 385
QY 195 KTENLVPWGLNL 206

RESULT 12
ID NAHL_CRIGR STANDARD; PRT; 822 AA.
AC P48761;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE SODIUM/HYDROGEN EXCHANGER 1 (NA(+)/H(+)) EXCHANGER 1 (NHE-1).
GN SLC9A1 OR NHE1.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 93192332.
RA COUNILLON L., POUVSEBUR J.;
RT "Nucleotide sequence of the Chinese hamster Na+/H+ exchanger NHE1.";
RL Biochim. Biophys. Acta 1172:343-345(1993).
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED

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CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL  
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD  
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL  
 CC TRANSDUCTION.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED (POSSIBLE).  
 CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.  
 CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC  
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.  
 CC -1- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE  
 CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.  
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 CC -----  
 DR EMBL; X68970; CAA48771.1; -  
 DR PFAM; PF00999; Na\_H\_Exchange; 1.  
 KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;  
 KW Multigene family; Phosphorylation.  
 FT DOMAIN 1 12  
 FT DOMAIN 13 32  
 FT DOMAIN 33 105  
 FT DOMAIN 106 127  
 FT DOMAIN 128 130  
 FT TRANSMEM 131 150  
 FT DOMAIN 151 162  
 FT TRANSMEM 163 183  
 FT DOMAIN 184 188  
 FT TRANSMEM 189 210  
 FT DOMAIN 211 230  
 FT TRANSMEM 231 251  
 FT DOMAIN 252 260  
 FT TRANSMEM 261 282  
 FT DOMAIN 283 301  
 FT TRANSMEM 302 322  
 FT DOMAIN 323 336  
 FT TRANSMEM 337 357  
 FT DOMAIN 358 388  
 FT TRANSMEM 389 410  
 FT DOMAIN 411 416  
 FT TRANSMEM 417 438  
 FT DOMAIN 439 452  
 FT DOMAIN 453 473  
 FT DOMAIN 474 482  
 FT TRANSMEM 483 503  
 FT DOMAIN 504 822  
 FT CARBOHYD 374 374  
 SQ SEQUENCE 822 AA; 92003 MW; 17073216 CRC32;  
 Query Match 9.2%; Score 142; DB 1; Length 822;  
 Best Local Similarity 26.5%; Pred. No. 2,05e-03;  
 Matches 35; Conservative 40; Mismatches 46; Indels 11; Gaps 9;  
 Db 262 LVFGESLLNDVTVVLYHLFEFANYDSIGSD-IFLGFSLFFVVALGGVGVVY-GVI 319  
 Qy 82 LIFG--LL-AVIGTFPIFAGKGGKAVATSGVIFGAPICLYLAIFFGALYLSM 137  
 Db 320 AAFSTFTSHIRVIEPLVF-LYSYMYLISAEFLHSGIMALIASGVWRPVE-ANISH 377  
 Qy 138 ISLSS-VTASIAAVIGLVLLPLFGFILSYDLSF-TAIIAL-ASLIIRHKNRIAKN 194  
 Db 378 KSHTTIKYFLKM 389  
 Qy 195 KTNLVPWGLNL 206  
 RESULT 13  
 ID NAH1\_RABIT STANDARD; PRT; 816 AA.

AC P23791;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE SODIUM/HYDROGEN EXCHANGER 1 (NA(+)/H(+)) EXCHANGER 1) (NHE-1).  
 GN SLG9A1 OR NHE1.  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-ILEAL VILLOS;  
 RX MEDLINE; 91293066.  
 RA TSE C.-M., MA A.I., YANG V.W., WATSON A.J.M., LEVINE S.,  
 RA MONTROSE M.H., POTTER J., SARDET C., POYSESSEUR J., DONOWITZ M.;  
 RT "Molecular cloning and expression of a cDNA encoding the rabbit ileal  
 RT villus cell basolateral membrane Na+/H+ exchanger.";  
 RL EMBL J. 10:1957-1967(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-KIDNEY;  
 RX MEDLINE; 92096447.  
 RA HILDEBRANDT F., PIZZONIA J.H., REILLY R.F., REBOUCAS N.A.,  
 RA SARDET C., POYSESSEUR J., SLAYMAN C.W., ARONSON P.S., IGARASHI P.;  
 RT "Cloning, sequence, and tissue distribution of a rabbit renal Na+/H+  
 RT exchanger transcript.";  
 RL Biochim. Biophys. Acta 1129:105-108(1991).  
 RN [3]  
 RP SEQUENCE OF 472-816 FROM N.A.  
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-HEART MUSCLE;  
 RX MEDLINE; 91138752.  
 RA FLIEGEL L., SARDET C., POYSESSEUR J., BARR A.;  
 RT "Identification of the protein and cDNA of the cardiac Na+/H+  
 RT exchanger.";  
 RL FEBS Lett. 279:25-29(1991).  
 CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED  
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL  
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD  
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL  
 CC TRANSDUCTION.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: KIDNEY AND INTESTINE.  
 CC -1- PTM: PHOSPHORYLATED (POSSIBLE).  
 CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.  
 CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC  
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.  
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 CC -----  
 DR EMBL; X59935; CAA42558.1; -  
 DR EMBL; X61504; CAA43721.1; -  
 DR EMBL; X56336; CAA39881.1; -  
 DR PIR; S13926; S13926.  
 DR PIR; S16328; S16328.  
 KW PFAM; PF00999; Na\_H\_Exchange; 1.  
 KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;  
 KW Multigene family; Phosphorylation.  
 FT DOMAIN 1 15  
 FT TRANSMEM 16 35  
 FT DOMAIN 36 107  
 FT TRANSMEM 108 127  
 FT DOMAIN 128 129  
 FT TRANSMEM 130 149  
 FT DOMAIN 150 154  
 FT TRANSMEM 155 174  
 FT DOMAIN 175 191  
 FT TRANSMEM 192 211

FT DOMAIN 212 227 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 228 247 MSA (POTENTIAL).  
 FT DOMAIN 248 256 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 257 276 M5B (POTENTIAL).  
 FT DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 295 315 M6 (POTENTIAL).  
 FT DOMAIN 316 338 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 339 358 M7 (POTENTIAL).  
 FT DOMAIN 359 386 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 387 406 M8 (POTENTIAL).  
 FT DOMAIN 407 410 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 411 430 M9 (POTENTIAL).  
 FT DOMAIN 431 480 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 481 500 M10 (POTENTIAL).  
 FT DOMAIN 501 816 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 75 75 POTENTIAL.  
 FT CARBOHYD 370 370 POTENTIAL.  
 FT CONFLICT 242 242 V -> A (IN REF. 2).  
 FT CONFLICT 569 569 K -> E (IN REF. 2).  
 SQ SEQUENCE 816 AA; 90717 MW; 6315C4BF CRC32;

Query Match 9.1%; Score 141; DB 1; Length 816;  
 Best Local Similarity 27.3%; Pred. No. 2.61e-03;  
 Matches 36; Conservative 37; Mismatches 48; Indels 11; Gaps 9;

Db 258 LVFGESLLNDVAVVLYHLFEFANVDHVGI-VDIVLGLSFFVVALGGVGVVY-GVI 315  
 QY 82 LIFG--LL--AVIGHTPFIFAGKGVATSGVIFGAPICFLYLAIFFGALYLSM 137  
 Db 316 AAFSTRTAHIRVIEPLFVF-LYSYMAVLSAELFHSGLMIALIASGVVMPYVE-ANISH 373  
 QY 138 ISLS-VTASIAAVIGVLLPLFGFILSNYSLSF-IAIILAL-ASLIIRHKDNIARIKN 194  
 Db 374 KSHTTIKYFLKM 385  
 QY 195 KTNLVPWGLNL 206

RESULT 14  
 ID NAHL\_PIG STANDARD; PRT; 818 AA.  
 AC P48762;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE SODIUM/HYDROGEN EXCHANGER 1 (NA(+)/H(+)) EXCHANGER 1 (NHE-1).  
 GN SLC9A1 OR NHE1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92087905.  
 RA REILLY R.F., HILDEBRANDT F., BIEMESDERFER D., SARDET C.,  
 RA POUYSSEGUER J., ARONSON P.S., SLAYMAN C.W., IGARASHI P.;  
 RT "CDNA cloning and immunolocalization of a Na(+)-H+ exchanger in  
 RT LLC-PK1 renal epithelial cells.";  
 RL Am. J. Physiol. 261:F1088-F1094 (1991).  
 CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED  
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL  
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD  
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL  
 CC TRANSDUCTION.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED (POSSIBLE).  
 CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.  
 CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC  
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.  
 CC -1- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE  
 CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.  
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 -----  
 CC EMBL; M89631; AAA31092.1; -;  
 CC EMBL; S71135; AAB20633.1; -;  
 CC PFAM; PF00999; Na\_H\_Exchange; 1.  
 KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;  
 KW Multigene family; Phosphorylation.  
 FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 12 31 A (M1) HYDROPHOBIC.  
 FT DOMAIN 32 101 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 102 123 B (M2) HYDROPHOBIC.  
 FT DOMAIN 124 126 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 127 146 C (M3) (POTENTIAL).  
 FT DOMAIN 147 158 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 159 179 D (M4) (POTENTIAL).  
 FT DOMAIN 180 184 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 185 206 E (M5) (POTENTIAL).  
 FT DOMAIN 207 226 F (M5A) (POTENTIAL).  
 FT TRANSMEM 227 247 G (M5B) (POTENTIAL).  
 FT DOMAIN 248 256 H (M6) (POTENTIAL).  
 FT TRANSMEM 257 278 I (M7) (POTENTIAL).  
 FT DOMAIN 279 297 J (M8) (POTENTIAL).  
 FT TRANSMEM 298 318 K (M9) (POTENTIAL).  
 FT DOMAIN 319 332 L, HYDROPHOBIC.  
 FT TRANSMEM 333 353 M (M10) (POTENTIAL).  
 FT DOMAIN 354 384 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 385 406 N (M11) (POTENTIAL).  
 FT DOMAIN 407 412 O (M12) (POTENTIAL).  
 FT TRANSMEM 413 434 P (M13) (POTENTIAL).  
 FT DOMAIN 435 448 Q (M14) (POTENTIAL).  
 FT TRANSMEM 449 469 R (M15) (POTENTIAL).  
 FT DOMAIN 470 478 S (M16) (POTENTIAL).  
 FT TRANSMEM 479 499 T (M17) (POTENTIAL).  
 FT DOMAIN 500 518 U (M18) (POTENTIAL).  
 FT CARBOHYD 370 370 POTENTIAL.  
 FT CONFLICT 683 683 H -> Y (IN AAB20633).  
 SQ SEQUENCE 818 AA; 90987 MW; 771B7051 CRC32;

Query Match 9.1%; Score 140; DB 1; Length 818;  
 Best Local Similarity 26.5%; Pred. No. 3.31e-03;  
 Matches 35; Conservative 38; Mismatches 48; Indels 11; Gaps 9;

Db 258 LVFGESLLNDVAVVLYHLFEFANVDHVGI-VDIVLGLSFFVVALGGVGVVY-GVI 315  
 QY 82 LIFG--LL--AVIGHTPFIFAGKGVATSGVIFGAPICFLYLAIFFGALYLSM 137  
 Db 316 AAFSTRTSHIRVIEPLFVF-LYSYMAVLSAELFHSGLMIALIASGVVMPYVE-ANISH 373  
 QY 138 ISLS-VTASIAAVIGVLLPLFGFILSNYSLSF-IAIILAL-ASLIIRHKDNIARIKN 194  
 Db 374 KSHTTIKYFLKM 385  
 QY 195 KTNLVPWGLNL 206

RESULT 15  
 ID NAHL\_RAT STANDARD; PRT; 820 AA.  
 AC P26431;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE SODIUM/HYDROGEN EXCHANGER 1 (NA(+)/H(+)) EXCHANGER 1 (NHE-1).  
 GN SLC9A1 OR NHE1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-SPRAGUE-DAWLEY; TISSUE-HEART;  
 RX MEDLINE; 92250539.



